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Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Title:
Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
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Match
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 ,
  124.6.09 (1.00 to 1.00 to 1.00
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pir2:*
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GenCore version 4.5
(c) 1993 - 2000 Com
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T42722
T42722
B33501
B350194
A35094
A3501477
T47237
F747237
F74723
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A41919
A41604
S21801
H69378
I84737
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hypothetical prote
cell-cycle-depende
                                                                             myosin heavy chain myosin heavy chain conserved hypothet kinesin heavy chai
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tanabin - African
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smooth muscle myos
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transport protein
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                          chain
slime
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45		43									34	33	32	31	
153.5	154	154	154.5	154.5	154.5	154.5	154.5	154.5	154.5	154.5	155	155	155	156	156.5
14.3	14.3	14.3	14.4	14.4	14.4	14.4	14.4	14.4	14.4	14.4	14.4	14.4	14.4	14.5	14.6
1938	1976	896	2411	2385	1201	1201	1175	1175	1133	380	1690	1156	484	412	1509
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MWKW1	A59252	S43074	в32491	A32491	B35815	A35815	D35815	C35815	T22976	T25454	T13030	в70356	S60943	S07537	A27224
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myosin heavy	myosin heavy	epidermal growth	myo	myo	myosin heavy	myo	myo	myc	hyg	hyp	microtubule bindi	chr	RUD3 proteir	mус	myc

ALIGNMENTS

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myosin heavy chain - Entamoeba histolytica C;Species: Entamoeba histolytica C;Date: 15-oct-1999 #sequence_revision 15-c;Accession: T18296 R;Guillen, N. submitted to the EMBL Data Library, Februa: A;Reference number: Z18865 A;Accession: T18296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Genetics:
A;Gene: TRIP
A;Introns: 33/2; 52/3; 80/3; 94/1; 136/3; 168/2; 206/2; 235/3; 265/3; 310/1; 352/3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R:Cottage, A.J.; Clark, M.; Hawker, K.; Umrania, Y.; Wheller, D.; Bishop, M.; Elgar, FEBS Lett. 443, 370-374, 1999
A;Title: Three receptor genes for plasminogen related growth factors in the genome of A;Reference number: Z20880; MUID:99148833
A;Accession: T30807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Species: Fugu rubripes
C;Date: 02-Sep-2000 #sequence_revision 02-Sep-2000 #text_change 02-Sep-2000
C;Accession: T30807
                                                                                                                                                                                       RESULT
T18296
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A; Residues: 1-433 <COT>
A; Cross-references: EMBL: AJ010317;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TRAF interacting protein - Fugu rubripes
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                  178
                                                                                                                                                                                                                                                                                                                   183 TLNTELDQAKLELRSAQKDLQSADQEITSLRKK 215
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 IINKLFFDLAQEEENVLDAEFLKNELDSVKAQLSQKDREKRDSQAIIDTLRDTLEERNAT
                                                                                                                                                                                                              N
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  VESLQNALNKAEMLCSTLKKQMKFLEQRQDETKQAREEAHRLKCKMKTMEQIELLLQSQR
preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                            KALLELTKARDDMKSLQNDLTNAEKEISSLKKK 270
                                                                                                                                                                                                                                                                                                                                                                  AEVESMITDMGIGQAAVEQLSIYCISLKKEYDNLKGGLKSSNEMCEKLKREVLTSNNKLH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 522; DB 2;
Pred. No. 3.8e-22;
59; Mismatches 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NID:e1355235; PID:e1355237; PIDN:CAA09084.1
                                                              February 1997
                                                                                                                            15-Oct-1999 #text_change 08-Sep-2000
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RESULT 3
T16270
Protein F35D11.11 - Caenorhabditis elegans
hypothetical protein F35D11.11 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #tex
C:Accession: T16270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Molecule type: DNA
A;Residues: 1-2139 <GUI>
A;Cross-references: EMBL:L03534; NID:g1850912;
C;Genetics:
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A; Reference number: 218487
A; Accession: T16270
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C:Superfamily: myosin heavy chain; myosin motor
F;91-780/Domain: myosin motor domain homology <
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A; Introns:
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RESULT
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A;Experimental source: strain Bristol N2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-1827 <FUL>
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Best Local Similarity
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Best Local Similarity
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                                                                                                                                                                                                                                                                                      G
                                                                                                                                                                                                                                                                                                                                                                                                 CESP:F35D11.11
ns: 76/2; 131/3; 159/3; 185/3;
                                                                              DRLKKDLVSSRSKLKTLNTELDQAKLELRSAQKDLQSADQE-ITSLRKK 215
                                                                                                                                                                                                                                                                    NKLFFDLAQEEENVLD------AEFLKNELDSVKAQLSQKDREKRDSQAIIDTLR---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KTLNTELDQAKLELRSAQKDLQSADQEITSLRKKSDD
                                                                                                                                                KTMEQIEL-LLQSQRSEVEEMIRDMGVGQSAVEQLAVYCVSLKKEYENLKEARKATGELA
                                                                                                                                                                                 DKLTNELKQKGVTVDSLNEEI-----SSLKEQLNKSEKERKEELLRMEELEQKNEAEM
                                                                                                                                                                                                           ----DTLEERNATVESLQNALNKAEMLCSTLKKQM-KFLEQRQDETKQAREEAHRLKCKM 108
                                                                                                                                                                                                                                                 NEKYDDAARKNDALLEDVATWQEKYEQLKMELEEMNRRGQEKEREEADLRALLDDLRGNF 728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EALQKNLDLAQQEKAKATKDYRAADGELKSLMNELDD
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                                                ERLKEKM----RKELEKLNEQNDGDRAEWSNERNRLESSKNEAVTELQER
                                                                                                                KEEYEVKLQLAEKDRQGVENFGKEC---EARMNELTKIHEMLMEEHDQLKVDHLHTEEEV
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                                                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                   16.3%;
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27.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            52;
                                                                                                                                                                                                                                                                                                                                 Score 175.5; DB Pred. No. 0.024;
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Pred. No. 0.016;
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RESULT
T38077
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A;Note: repeat 15-160 and 200-340
C;Comment: This protein contains a coiled-coil and a globular domain at the carboxy-t C;Keywords: nucleoprotein; phosphoprotein
C;Keywords: nucleoprotein; phosphoprotein
F;465/Binding site: phosphate (Thr) (covalent) (by camp-dependent kinase) #st
F;825,826,838/Binding site: phosphate (Ser) (covalent) (by cAmp-dependent kinase) #status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R:Li, Q.; Ke, Y.; Kapp, J.A.; Fertig, N.; Medsger Jr., T.A.; Joshi, H.C. Biochen. Biophys. Res. Commun. 212, 220-228, 1995
A;Title: A novel cell-cycle-dependent 350-kDa nuclear protein: C-terminal A;Reference number: PC4035; MUID:95336446
A;Accession: PC4035
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c;Species: Homo sapiens (man)
C;Date: 08 -Aug-1995 #sequence_revision 19-Oct-1995 #text_change
C;Accession: PC4035
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A; Residues: 1-1017 <LIQ>
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                                                                                                                                                                         LLKGRVENLERELEIARTNQEHAALEAENSKGEVETLKAKIEGMTQSLRGLELDVVTIRS
                                                                                                                              KLKTLNTELDQ-----AKLEL--RSAQKDLQSADQEITSLRKKS
                                                                                       EKEDLTNELQKEQERISELETINSSFENTLQEKEQEKVQMKEKS
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C;Genetics: A;Gene: SPDB:SPA A;Map position: A; Dia Luc. F. DNA
A; Molecule type: DNA
A; Residues: 1-1957 <CON>
A; Cross references: EMBL: Z70690; PIDN: CAA94624.1;
A; Cross references: strain 972h-; cosmid c1F3 hypothetical coiled-coil protein - fission yeast (Schizosaccharomyces pombe) C;Species: Schizosaccharomyces pombe C;Species: Schizosaccharomyces pombe C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999 C;Accession: T38077 A; Reference number: Z21767 A; Accession: T38077 R; Connor, R.; Churcher, C.M.; submitted to the EMBL Data Lil A;Status: preliminary; translated Query Best L Accession: T38077 Matches Local Match Local Similarity SPDB:SPAC1F3.06c Conservative 15.8%; Library, Barrell, B.G.; Rajandream, brary, April 1996 54; Score 169.5; DB Pred. No. 0.055; from Mismatches GB/EMBL/DDBJ GSPDB:GN00066; 96; 2 Indels Length M.A.; 1957; Walsh, 37; SPDB:SPAC1F3.06c Gaps 4

Дb

1386

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male-enhanced antigen-2 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 11-Jan-2000 #sequence_revision
C:Accession: T42722
R:Kondo, M.; Sutou, S.
DNA Seq. 7, 71-82, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: DBJ:D85924; NID:g1945079; PIDN:BAA19691.1;
A;Experimental source: smooth muscle
C;Comment: This protein plays a role in smooth muscle cell cont;
C;Superfamily: myosin heavy chain; myosin motor domain homology
C;Keywords: nucleotide binding; P-loop
E;88-771/Domain: myosin motor domain homology <MMOT>
F;178-185/Region: nucleotide-binding motif A (P-loop)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R:Hasegawa, K.; Arakawa, E.; Oda, S.; Matsuda, Y. Biochem. Biophys. Res. Commun. 232, 313-316, 1997 A;Title: Molecular cloning and expression of murine smooth muscle A;Reference number: JC5420; MUID:97242182 A;Accession: JC5421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       smooth muscle myosin heavy chain 2 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 10-Jun-1997 #sequence_revision 18-Jul-1997
C;Accession: JC5421
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A; Residues: 1-1938 <HAS>
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Pred. No. 0.058;
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                                                        11-Jan-2000 #text_change
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DLMQLQEDLAAAERARKQADLEKEELAEELASSLSGRNALQDEKRRLEARIAQLEEELEE

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myosin heavy chain 2, smooth muscle - rabbit (fragment) () Species: Oryctolagus cuniculus (domestic rabbit) C; Date: 08-Dec-1989 #sequence_revision 08-Dec-1989 #tex C; Accession: B3501; A31368 R.Nagai, R.; Kuro-o, M.; Babij, P.; Periasamy, M. J. Biol. Chem. 264, 9734-9737, 1989 A; Title: Identification of two types of smooth muscle m A; Reference number: A33501; MUID:89255335
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                                                                                                                                      C; Superfami
C; Keywords:
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δõ
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R;Nagai, R.; Larson, D.M.; Periasamy, M.
Proc. Natl. Acad. Sci. U.S.A. 85, 1047-1051,
A;Title: Characterization of a mammalian smooth
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                                                                                                                                                    A;Residues: 1-484 <NA2>
A;Cross-references: GB:J03614; NID:g165517; PIDN:AAA31406.1;
C;Superfamily: myosin heavy chain; myosin motor domain homolo
                                                                                                                                                                                             A; Molecule type: mRNA
A; Residues: 1-484 <NA
                                                                                                                                                                                                                                    A; Reference number: A; Accession: A31368
                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: mRNA
A; Residues: 1-484 <NAG>
                                                                                                                                                                                                                                                                                                                                                                                                                             A; Reference number: A33501;
                                                                                                                                                                                                                                                                                                                                                                                                             A; Accession: B33501
                                                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary
                                                             Query Match
Best Local :
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Best Local Similarity
                                          Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          192 KLELRSAQKDLQSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              703 LKATKKRLDSEMKELRQELIKLQGEKKTVEVEHSRLQKDMSLVHQQMAELEGHLQSVQKE 762
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DLAQEEENVLDAEFLKNELDSVKAQLSQK------DREKRDSQAIIDTLRDTLEE 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RDEMEIHLQSLKFDKEQMIALTEANETLKKQIEELQQEAKKAITEQKQKMKRLGSDLTSA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    leucine zipper
                                                                                                                                      muscle; smooth muscle
                                                             Similarity
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23.8%;
                                                         15.6%;
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                                        52;
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                                                           Score 168; DB 2
Pred. No. 0.016;
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                                                                           Length 484
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                                                                                                                                                                                                                                                                            heavy chain
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Proc. Natl. Acad. Sci. U.S.A. 87, 6316-6320, 1990
A;Title: Complete sequence of the Drosophila nonmuscle myo A;Reference number: A36014; MUID:90349606
A;Accession: A36014
A;Molecule type: mpmn
A;Molecule type: mpmn
                                                                                                                                 myosin heavy chain, nonmuscle - fruit fly (Drosophila melanogaster) N;Contains: myosin ATPase (EC 3.6.1.32) C;Species: Drosophila melanogaster C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 19-C;Accession: A36014; B36014
R;Ketchum, A.S.; Stewart, C.T.; Stewart, M.; Kiehart, D.P.
                                                                                                                                                                                                                                          RESULT
A36014
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A; Cross-references:
                A; Molecule type:
A; Residues: 1-201
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A; Residues: 1-1203 <HIR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       chromosomal protein; DNA condensation;
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                                                                                                nonmuscle myosin
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                                                                                                 heavy-chain transcript:
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A;Gene: zip
A;Cross-references: FlyBase:FBgn0005634
A;Cross-references: FlyBase:FBgn0005634
A;Introns: 10/3; 90/3; 162/3; 215/1; 255/3; 263/3; 303/3; 334/3; 1248/1; 1349/3; 1526
C;Superfamily: myosin heavy chain; myosin motor domain homology
C;Superfamily: myosin heavy chain; myosin motor domain homology
C;Superfamily: myosin heavy chain; myosin motor binding; P-loop
F;135-855/Domain: myosin motor domain homology <MMOT>
F;135-855/Domain: myosin motor domain homology <MMOT>
F;225-232/Region: nucleotide-binding motif A (P-loop)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         myosin II heavy chain, non-muscle - fruit fly (Drosophila melanogaster) (; Species: Drosophila melanogaster C; Date: 19-unl-196 #sequence_revision 26-Jul-1996 #text_change 02-Feb-2001 C; Accession: S61477; S65349 R; Mansfield, S.G.; Al-Shirawi, D.Y.; Ketchum, A.S.; Newbern, E.C.; Kiehart, J. Mol. Biol. 255; 98-109, 1996 A; Title: Molecular organization and alternative splicing in zipper, the gen A; Reference number: S61477; MUID:96144835
                                                                                                                                                                                                                                                                                                 A;Molecule type: DNA
A;Residues: 1-1908,'NL',1911-2057 <MAW>
A;Cross-references: EMBL:U35816; NID:g1141789;
                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: EMBL:U35816
R;Mansfield, S.G.; Al-Shirawi, D.Y.; Ketchum,
submitted to the EMBL Data Library, September
A;Reference number: S65349
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S61477
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A;Cross-references: FlyBase:FBgn0005634
A;Cross-references: FlyBase:pBgn0005634
C;Superfamily: myosin heavy chain; myosin motor domain homology
C;Keywords: actin binding; alternative splicing; ATP; coiled coil; hydr
C;Keywords: actin binding; alternative splicing; ATP; coiled coil; hydr
C;Keywords: myosin heavy chain, form I #status predicted <MA1>
F;1-2017/Product: myosin heavy chain, form II #status predicted <MA2>
F;135-815/Domain: myosin motor domain homology <MVOT>
F;135-815/Domain: myosin motor domain homology <MVOT>
F;225-232/Region: nucleotide-binding motif A (P-loop)
F;598-631/Region: actin binding #status predicted
F;808-131/Pomain: coiled coil #status predicted
F;808-1328/Region: Sciled coil #status predicted
F;808-1328/Region: Sciled coil #status predicted
F;808-1328/Region: Sciled coil #status predicted
                                                                                                                                                                                                                                                                      C; Genetics:
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F;176/Modified site: N6.N6.N6-trimethyllysine (Lys)
F;231/Binding site: ATP (Lys) #status predicted
F;745,755/Active site: Cys #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                       A; Accession: S65349
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A; Residues: 1-2057 <MAN>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  214 KK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        줐
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KATGELADRLKKDLVSSRSKLKTL - - - NTELDQAKLELRSAQKD - - - - LQSADQEITSLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---LKCKMKTMEQIELLLQSQRSEVEEMIRDMGVGQSAVEQLAVYCVSLKKEYENLKEAR 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IERARSELQEKCTKLQQEAENITNQLEEAELKASAAVKSASNMESQLTEAQQLLEEETRQ 1374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IDTLRDTLEER----NATVESLQNALNKAEMLCSTLKKOMKFLEQRQDETKQAREEAHR- 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KELEEGKKRLNKDIEALERQVKELIAQNDRLDKSKKKIQSELEDATIELEAQRTKVLELE 1491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   D.Y.; Ketchum, A.S.; Newbern, E.C.; Kiehart, D.P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  47;
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Pred. No. 0.089;
7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A.S.;
                                                                                                                                                                                                                                                                                                        PIDN: AAB09049.1;
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                                                                                                                                                                                                                                                                                                        PID: g1572481
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myosin II heavy chain [imported] - Naegleria fowleri (fragment) C;Species: Naegleria fowleri C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Description: Codon usage in Naeg
A;Reference number: Z24413
A;Accession: T47737
A;Status: preliminary; translated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Accession: T47237
R;Shaw, D.R.; Sullivan, P.K.; Marciano-Cabral, F.; submitted to the EMBL Data Library, December 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    δõ
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A;Experimental source: strain LEE mp; cell type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: mRNA
A; Residues: 1-746 <SHA>
 hypothetical
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Best Local
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                                                                                                                                                                                                        GVKSERDRLNKDLNNTSGDMNGLKRQLDESNNLVAKLKAEIQKLQKDLSDHHGDREETEE
                                                                                                                                                                                                                                                                                                     ATVESLQNALNKAEMLCSTLKKQMKFLEQRQDETKQA-REEAHRLKCKMKTMEQIELLLQ 119
                                                                                                                                                                                                                                                                                                                                       KQLQNELQNERTNLQKMKSENERLQRELEEMKRSLSDKQNESTSLDSKVKSLEDKIRELT
                                                                               EMERVOSESEN
                                                                                                           EITSLRKKSDD
                                                                                                                                           QLDALRKQLQELTSRLSDANQKTQQEAASRQNLESENNRLKSEVSRLREDLQNENRRLKQ
                                                                                                                                                                         LADRLKKDLVSSRSKL--
                                                                                                                                                                                                                                          SQRSEVEEMIRDMG----
                                                                                                                                                                                                                                                                      ALLETERSSKIDLDKKRSKMDKEVKRLAQQLQETEQALKGETQKKNDADNRVKQLESELQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IERARSELQEKCTKLQQEAENITNQLEEAELKASAAVKSASNMESQLTEAQQLLEEETRQ 1414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IDTLRDTLEER----NATVESLQNALNKAEMLCSTLKKQMKFLEQRQDETKQAREEAHR-
                                                                                                                                                                                                                                                                                                                                                                                                      1 Similarity
57; Conserv
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protein F13011.30 [imported] - Arabidopsis thaliana
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22.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                  Score 164.5; DE 
Pred. No. 0.039; 
7; Mismatches 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 166; DB Pred. No. 0.09;
                                                                                                                                                                                                                                        ----VGQSAVEQLAVYCVSLKKEYENLKEARKATGE 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
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                                                                                                                                                                       -KTLNTELDQAKLELRSAQKDLQSAD----Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  type amoeba
                                                                                                                                                                                                                                                                                                                                                                                                                                DВ 2;
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Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H. ansen, N.F.; Hughes, B.; Huizar, L. Nature 408, 816-820, 2000

A.Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, C.Z.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.R.; Cla, M.; Rooney, T.; Rowley, D.; Sakano, H.

A.Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A.;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A.;Accession: F96673

A.;Accession: F96673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      transport protein USO1 - yeast (Saccharomyces cerevisiae) N;Alternate names: protein D2552; protein YDL058w C;Species: Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Qy
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A; Map position:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C;Accession: F96673
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White
A;Molecule type: DNA
A;Residues: 1-389,'TA',392-724,'S',726-1790 <NAK>
A;Cross-references: GB:X54378; NID:94777; PIDN:CAA38253.1; PI
A;Note: the authors translated the codon ACT for residue 768
                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Saccharomyces cerevisiae
C;Date: 12-Jul-1996 #sequence_revision
C;Accession: S67593; A38455; S30782
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                                                                                                                                                                              A;Experimental source: strain S288C
R;Nakajima, H.; Hirata, A.; Ogawa, Y.; Yonehara, T.; Yoda, K.; Yamasaki,
J. Cell Biol. 113, 245–260, 1991
                                                                                                                                                                                                                                                                                                                                                                        R; Bloecker, H.; Brandt, P. submitted to the Protein S
                                                                                                                                 A; Title: A cytoskeleton-related gene, USO1, A; Reference number: A38455; MUID:91185402
                                                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-1790 <BLO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-1313 <
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                                                                                                             A; Accession: A38455
                                                                                                                                                                                                                                                   A;Cross-references: EMBL:274106; NID:g1431058; PID:e253003; PID:g1431059; MIPS:YDL058
                                                                                                                                                                                                                                                                                                                           A; Accession: S67593
                                                                                                                                                                                                                                                                                                                                                  A; Reference number: S67587
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 67; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                66
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Dsition: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GB:AE005173;
                                                                                                                                                                                                                                                                                                                                                                          Sequence Database,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15.2%; 22.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NID:g5042434; PIDN:AAD38273.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 163; DB 2
Pred. No. 0.083;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                              12-Jul-1996 #text_change 21-Jul-2000
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                                                                                                                                                          required
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              ; PID:g4778
768 as Ile
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GSPDB:GN00141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---EEA 101
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A; Molecule type: DNA
A; Residues: 1-2116 < MAR>
A; Residues: 1-2116 < MAR>
A; Cross-references: GB:M14628; GB:M11938; NID:g167834; PIDN:AAA33227.1; PID:
A; Cross-references: GB:M14628; MID:g167884; PIDN:AAA33227.1; PID:
A; Cross-reference number: A24728; MUID:86016788
A; Reference number: A24728; MUID:86016788
A; Accession: A24728
A; Molecule type: mRNA
A; Residues: 2035-2116 < DEL>
A; Magle, G:; Noegel, A.; Scheel, J.; Gerisch, G.
FEBS Lett. 227, 71-75, 1988
A; Title: Phosphorylation of threonine residues on cloned fragments of the Di A; Reference number: S00250; MUID:88112226
A; Status: nucleic acid sequence not shown
A: Molecule type: NNA
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1734-1893 <WAG>
A; Residues: 1734-1893 <WAG>
C; Comment: The rod domain is highly periodic, containing a pattern of 7-residue
C; Superfamily: myosin heavy chain; myosin motor domain homology
C; Keywords: actin binding; ATP; colled coil; hydrolase; nucleotide binding; P-lo; F; 1-818/Domain: globular head <HEDD
F; 1-818/Domain: myosin motor domain homology <MMOT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A26655

A26655

MyOsin heavy chain [similarity] - slime mold (Dictyostelium discoideum)
N;Contains: myosin ATPase (EC 3.6.1.32)
C;Species: Dictyostelium discoideum
C;Date: 05-Oct-1988 #sequence_revision 05-Oct-1988 #text_change 02-Feb-2001
C;Accession: A26655, A24728; S00250
R;Warrick, H.M.; De Lozanne, A.; Leinwand, L.A.; Spudich, J.A.
Proc. Natl. Acad. Sci. U.S.A. 83, 9433-9437, 1986
A;Title: Conserved protein domains in a myosin heavy chain gene from Dictyo.
A;Reference number: A26655; MUID:87092266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Map position: 4L

C; Keywords: coiled coil; transmembrane protein

F; 326-342/Domain: transmembrane #status predicted

F; 394-410/Domain: transmembrane #status predicted

F; 617-633/Domain: transmembrane #status predicted
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A; Cross-references: SG
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A;Residues: 71-846,'E',848-923,'K',925-1252,'I',1254-1318,'V',1320-1460,'S',1462-1580,
A;Cross-references: EMBL:L03188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R; Hostetter, M.K.; Herman, submitted to the EMBL Data A; Description: An integrin A; Reference number: $30782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C; Genetics:
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Best Local S
Matches 51
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ELLEEKQNTIKS--LQDEI-----LSYKDKITRNDEKLLSIERDNKRD----LESLKEQ 1471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LNTELDOAKLELRSAOKDLQSADQEITSLRKKSDD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ETIRKSDEKLEQ-----SKKSAEEDIKNLQHEKSDLISRINESEKDIEELKSKLRIEAK 1579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SGSELETVKQELNNAQEKIRINAEENTVLKSKLED 1614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RDMGVGQSAVEQLAVYCVSLKKEYENLKEARKATGELADRL---KKDLVSSRSKLK---T 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LNKAEMLCSTLKKOMKFLEORODETKOAREEAHRLKCKMKTMEQIELLLOSORSEVEEMI 129
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23.7%;
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Library, February 1993
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Pred. No. 0.11;
7; Mismatches
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                                               P-loop; phos
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A; Molecule type: mRNA
A; Residues: 1-1938 (NYI)
A; Cross-references: GB:X55714; NID:g5611; PIDN:CAA39247.1; PID:g5612
C; Superfamily: myosin heavy chain; myosin motor domain homology
C; Keywords: actin binding; ATP; coiled coil; hydrolase; muscle contra
F; 86-763/Domain: myosin motor domain homology (MMOT)
F; 176-183/Region: nucleotide binding motif A (P-loop)
F; 547-586/Region: actin binding #status predicted
F; 633-675/Region: actin binding #status predicted
F; 836-1938/Domain: coiled coil #status predicted
F; 836-1276/Region: S2
F; 836-1276/Region: S2
F; 836-1276/Region: S2
                                                                                                                                                                                                                                                                                                                                                                                                                      F;1277-1938/Région: light meromyosin F;182/Binding site: ATP (Lys) #status predicted F;693,703/Active site: Cys #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Reference number: A; Accession: A40997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N;Contains: myosin ATPase (EC 3.6.1.32)
C;Species: Aequipecten irradians
C;Date: 31-Dec-1993 *sequence_revision 31-Dec-1993 *text_change
C;Accession: A40997; S13557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Nyitray, L.; Goodwin, E.B.; Szent-Gyoergyi, A.G.
J. Blol. Chem. 266, 18469-18476, 1991
A;Title: Complete primary structure of a scallop striated
A;Reference number: A40997; MUID:92011595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       F;179-186/Region: nucleotide-binding motif A (P-loop) F;819-2116/Domain: alpha-helical rod <ROD>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   myosin heavy chain,
                                                                                                                                                                                                                                                                                                  Query Match
Best Local S
Matches 73
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1026
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                                                                                                                                                                                                904 KLIMQKADFESQIKELEERLLDEEDAAADLEGIKKKMEADNANLKKDIGDLENTLQKAEQ
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                                            75
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 ATVESLQN-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LALENLQNQKRSVEEKVRDLEEELQEEQKLRNTLEKLKKKYEEELEEMKRVNDG-----
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                                                                                               DKAHKDNQ--ISTLQGEISQQDEHIGKLNKEKKALEEANKKTSDSLQAEEDKCNHLNK--
                                                                                                                            DREKRDSQAIIDTL-----NALNKAE 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ELRSAQKDLQS----ADQEITSLRKKSD
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-LKAKLEQALDELEDNLEREKKVRGDVEKAKRKVEQDLKSTQENVEDLERVKR-ELEENV 1077
                                       MLCSTLKKQMKFLEQRQDETKQAREEAHRLKCKMK-----TMEQIELLLQSQRSEVEEMI 129
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73; Conser
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24.5%;
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                                                                                                                                                                                                                                                                                                     50;
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                                                                                                                                                                                                                                                                                                  Score 162; DB Pred. No. 0.14; 0; Mismatches
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Pred. No. 0.15;
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smooth muscle myosin heavy chain isoform SM2 - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 13-Aug-1999
C;Accession: I52860
R;Aikawa, M.; Sivam, P.N.; Kuro-o, M.; Kimura, K.; Nakahara, K.; Takewaki, S.;
Circ. Res. 73, 1000-1012, 1993
A;Title: Human smooth muscle myosin heavy chain isoforms as molecular markers fareference number: I52860; MUID:94037315
A;Accession: I52860
                                                                                                                                                                                                                                                                                                                                  RESULT
JH0720
                                                                        A;Cross-references: GB:M99387; NID:g214816; A;Experimental source: tadpole head C;Keywords: intermediate filament
                                                                                                                                                                A; Title: A protein expressed in the growth A; Reference number: JH0720; MUID:92398961 A; Accession: JH0720
                                                                                                                                                                                                                                                        tanabin - African clawed frog
C;Speckes: Xenopus laevis (African clawed frog)
C;Date: 10-Jun-1993 #sequence_revision 10-Jun-1993
C;Accession: JH0720
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A; Residues: 1-296 < RES>
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                                                                                                                              A; Molecule type: mRNA
A; Residues: 1-1744 <HEM>
                                                                                                                                                                                                                     R; Hemmati-Brivanlou, A.; Mann, R.W.; Harland, Neuron 9, 417-428, 1992
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Query Match
Best Local Similarity
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Best Local
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23.8%;
14.9%;
24.3%;
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Pred.
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Pred. No. 0.
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160.5; DB No. 0.15;
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                                                                                                          PIDN: AAA49966.1;
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                   Length 1744;
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                                                                                                                                                                                                      vertebrate
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                 C;Date: 13-Jun-1983 #sequence_revision 19-May-2000 #text_change 19-Jan-2001 C;Accession: T20770; T21629; A93958; A93287; A21074; A02992
                                                 myosin heavy chain B [similarity] - Caenorhabditis N;Contains: myosin ATPase (EC 3.6.1.32) C;Species: Caenorhabditis elegans
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A; Experimental source: sex female C; Superfamily: myosin heavy chain; F;87-773/Domain: myosin motor domai
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mol. Biochem. Parasitol. 50, 255-260, 1992
A; Title: Comparison of the body wall myosin
A; Reference number: A59294; MUID:92158005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Accession: A.J.-.
R;Werner, C.; Rajan, T.V.
Parasitol. 50,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             skeletal myosin - nematode (Onchocerca volvulus)
N;Alternate names: major body wall myosin
C;Species: Onchocerca volvulus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Accession: A59294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 08-Sep-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: GB:M74066; NID:g159892; PIDN:AAA29420.1; PID:g159893
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local
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                                                                                                                                                                                                                                                                         1002
1171 NKKREAELAKLRRDLEEANMNHENQLAAIRKKHND
                                                                                                                                                                               1062 IGGELKVAQENMEEIE----RQRHEIESNLKKKETEAQAITARLEEEQDLVGKLKKQVNE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 136
                                                                                                                                                                                                                                                                                                                                                               942 DLSRSKKKIENDVENLKKSIAELETRLQKTDADKQSREQQIRTLQDEMQQQDENIAKLNK 1001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         193
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                                                                                                                                                                                                                                                                                                                    67
                                                                                                                                                                                                                                                                                                                                                                                                         10 DLAQEEENV-LDAEFLKNELDSVKAQLSQKDREKRDSQAIIDTLRDTLEERNATVESL--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         81
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LKKDLVSSRSKLKTLNTELDQAKLELRSAQKD-----LQSADQEITSLRKKSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GQLEAELEDILRDHEEEKALMEE---EIASFSQRLENFRVAPVAFKPVEVDDYARKLSEI 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QAEMVRDSIYEEIEFVKQRCLEEKQAREDA-----KKELSESKKLLEEETRAQIWLKERL 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ALEEEN----ELLRKEIHSLRSSKSERCWKKKHHEEMM-KLRDALDDGH---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AQEEENVLDAEFLKNELDSVKAQLSQKDREKRDSQAIIDTLRDTLEERNATVESLQNALN
                                                                                                                    LAVYCVSLKKEYENLKEARKATGELADRLKKDLVSSRSKLKTLNTELDQ-----
                                                                                                                                                                                                                                                                       EKKHQEEINRKLMEDLQVEEDKGNYSNKLKGKLEQSLDDLEDNLEREKRGRNEIEKQKRK 1061
                                                                                                                                                                                                                                                                                                                    ----QNALNKAEM----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----SEVEEMIRDMGVGQSAVEQLAVYCVSLKKEYENLKEARKA-----TGELADR 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KAEMLCSTLKKQMKFLEQRQDETKQAREEAHRLKCKMKTMEQIELLLQSQR------
                                                                                       TQNRITELEEELENERQSRSK----AERAKSDL---QRELEELGDRLDEQGGATAAQVEV 1170
                                                                                                                                                                                                                          ----LKCKMKTMEQIELLLQSQRSEVEEMIRD---------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               57;
                                        -AKLELRSAQKDLQSA----DQEITSLRKKSDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          יייביי יישמעץ chain; myosin motor domain myosin motor domain homology אייין myosin motor domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    56;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 160.5; D
Pred. No. 0.17;
                                                                                                                                                                                                                                                                                                               ---LCSTLKKQMKFLEQRQDETKQAREEAHR----
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1205
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A;Gene: unc-54; CESP:FI1C3.3

A;Map position: 1

A;Introns: 21/3; 64/3; 111/3; 264/1; 525/3; 951/2; 1747/3; 1819/3; 1894/3

C;Superfamily: myosin heavy chain; myosin motor domain homology

C;Keywords: actin binding; ATP; coiled coil; hydrolase; methylated amino in 84-775/Domain: myosin motor domain homology <MMOT>
F;84-775/Domain: myosin motor domain homology <MMOT>
F;174-181/Region: nucleotide-binding motif A (P-10op)
F;662-684/Region: actin binding #status predicted
F;766-780/Region: actin binding #status predicted
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F;1163-1963/Region: light meromyosin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Accession: A93287
A;Molecule type: DNA
A;Residues: 847-1333,'R',1335-1876,'L',1878-1963
A;Residues: 847-1333,'R',1335-1876,'L',1878-1963
R;Wills, N.; Gesteland, R.F.; Karn, J.; Barnett,
Cell 33, 575-583, 1983
A;Title: The genes sup-7 x and sup-5 III of Caeno
A;Reference number: A21074; MUID:83232892
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Rosidues: 1-61, 'EMSVIQ', 65-376, 'V', 378-1963 <KAR>
A; Residues: 1-61, 'EMSVIQ', 65-376, 'V', 378-1963 <KAR>
A; Residues: GB: J01050; NID: g156399; PIDN: AAA28124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Karn, J.; Brenner, S.; Barnett, L.
Proc. Natl. Acad. Sci. U.S.A. 80, 4253-4257, 1983
A;Title: Protein structural domains in the Caenorhabditis
A;Reference number: A93958; MUID:83273600
A;Accession: A93958
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                                                              В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;MCLachlan, A.D.; Karn, J.
Nature 299, 226-231, 1982
A;Title: Periodic Charge distributions in
A;Reference number: A93287; MUID:82272395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-1963 <WIL>
A; Cross-references: EMBL: Z81499;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 submitted to the EMBL Data
A; Reference number: Z19322
A; Accession: T20770
A; Status: translated from C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Cross-references: GB: V01494; GB: J01049; NID: g6783; PIDN: CAA24738.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Accession: A21074
A;Molecule type: DNA
A;Residues: 1873-1963 <WI3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: EMBL:283107; pA;Experimental source: clone F32A7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Experimental source: clone F11C3
                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local
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                                                                 1107
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                        182
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                                                                                                                                                                                                                                     INRKLMEDLQSEEDK-----GNHQNKVKAKLEQ------TLDDLEDSLEREKRA 1053
                      KTLNTELDQ
                                                            QALVSKLQRQIKDGQSRISE-----LEEELENERQSRSK----ADRAKSDL----QREL
                                                                                                     RSEVEEMIRDMGVGQSAVEQLAVYCVSLKKEYENLKEARKATGELADRLKKDLVSSRSKL 181
                                                                                                                                                                                          VESIQNALNKAEMICSTIKKOMKFLEORODET-KOAREEAHRIKCKMKTMEQIEILILOSO 121
                                                                                                                                                                                                                                                                                                                              59;
                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                              14.9%;
25.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Library, November 1996
                                                                                                                                                 --GELKIAQENIDESGRQRHDLENNLKKKESELHSVSSRLEDE
                                                                                                                                                                                                                                                                                                                            41;
                                                                                                                                                                                                                                                                                                                        Score 160.5; DI
Pred. No. 0.17;
41; Mismatches
                    AKLELRSAQKDLQSA - -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIDN:CAB04089.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PIDN: CAB05505.1; GSPDB: GN00019; CESP: F11C3
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                    -DQEITSLRKKSDD
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                                                                                                                                                                                                                                                                                                                          57;
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                                                                                                                           C; Genetics:
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A;Gene: GDB:KN51; AND
A;Cross-references: GDB:135352
A;Cross-references: GDB:135352
C;Superfamily: kinesin heavy chain; kinesin motor domain
C;Keywords: ATP; coiled coil; heterotetramer; hydrolase;
F;9-331/Domain: kinesin motor domain homology <KMOT>
F;9-331/Domain: kinesin motor domain homology <KMOT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A:Molecule type: mRNA
A:Residues: 1-1972 <HAS>
A:Residues: 1-1972 <HAS>
A:Cross-references: DDBJ:D85923; NID:g1945077; PIDN:BAA19690.1;
A:Experimental source: smooth muscle
C:Comment: This protein plays a role in smooth muscle cell contr
C:Superfamily: myosin heavy chain; myosin motor domain homology
C:Keywords: nucleotide binding; P-loop
F:88-771/Domain: myosin motor domain homology <MMOT>
F:178-185/Region: nucleotide-binding motif A (P-loop)
                                                                                                                                                                                                                                                                                                                                                                                                      C;Accession: A41919; S24603
R;Navone, F.; Niclas, J.; Hom-Booher, N.; Sparks,
J. Cell Biol. 117, 1263-1275, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Hasegawa, K.; Arakawa, E.; Oda, S.; Matsuda, Y. Biochem. Biophys. Res. Commun. 232, 313-316, 1997 A;Title: Molecular cloning and expression of murine A;Reference number: JC5420; MUID:97242182
                                                                                                                                                                                                                                             A; Molecule type: mRNA
A; Residues: 1-963 <NA
                                                                                                                                                                                                                                                                                                                                                A; Title: Cloning and expression of a human A; Reference number: A41919; MUID:92299683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Species: Mus musculus (house mouse)
C;Date: 10-Jun-1997 #sequence_revision
                                                                                                                                                                                                                 A;Cross-references:
                                                                                                                                                                                                                                                                                                                         A; Accession: A41919
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                                                                                                                                                                                                                                                                                                A;Status: nucleic acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            kinesin heavy chain -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Accession: JC5420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Species: Homo sapiens (man)
Date: 03-Mar-1994 #sequence_revision 03-Mar-1994 #text_change 19-Jan-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1921 VNALKSK 1927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    209 ITSLRKK 215
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nes 55; Conserv
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kinesin ATPase (EC 3.6.1.-)
                                                                                                                                                                                                                                          1-963 <NAV>
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22.3%;
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C:Superfamily: myosin heavy chain; myosin motor domain homology C:Keywords: actin binding; alternative splicing; ATP; coiled coi
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R;Babij, P.; Kelly, C.; Periasamy, M.
Proc. Natl. Acad. Sci. U.S.A. 88, 10676-10680, 1991
A;Title: Characterization of a mammalian smooth muscle A;Reference number: A41604; MUID:92073350
A;Accession: A41604
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: GB:M77812
R;Nagai, R.; Kuro-o, M.; Babij, P.; Periasamy, M.
J. Biol. Chem. 264, 9734-9737, 1989
A;Title: Identification of two types of smooth muscle myosin heavy A;Reference number: A33501; MUID:8925535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          myosin heavy chain, smooth muscle, long splice form - rabbit N;Contains: myosin ATPase (EC 3.6.1.32) C;Species: Oryctolagus cuniculus (domestic rabbit) C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 19-Jan-2001
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A;Residues: 1455-1972 <NAG>
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A; Residues: 1-1972 <BAB>
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                             DLAQEEENVLDAEFLKNELDSVKAQLSQK--
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Pred. No. 0.1;
48; Mismatches
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Pred. No. 0.
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A; Experimental source: brain
C; Superfamily: myosin heavy chain; myosin motor domain homology
C; Keywords: actin binding; ATP; coiled coil; hydrolase; methylai
F;84-763; Domain: myosin motor domain homology <MMOT>
F;84-163; Domain: myosin motor domain homology <MMOT>
F;174-181; Region: nucleotide-binding motif A (P-loop)
F;541-575; Region: actin binding #status predicted
F;653-675; Region: actin binding #status predicted
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Blochem. Blophys. Res. Commun. 175, 244-249, 1991
Blochem. A unique cellular myosin II exhibiting differential expression A;Reference number: PN0013; MUID:91151356
A;Accession: PN0013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       F;125/Modified site: N6,N6,N6-trimethyllysine (Lys) #status F;180/Binding site: ATP (Lys) #status predicted F;693,703/Active site: Cys #status predicted F;1916/Binding site: phosphate (Ser) (covalent) #status pred F;1916/Binding site: phosphate (Ser) (covalent) #status pred F;19143/Binding site: phosphate (Se
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           F:836-1999/Domain: coiled coil #status predicted F:836-1276/Region: S2 F:1277-1999/Region: light meromyosin
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C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993
C;Accession: S21801; pN0013; S18134
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A;Title: Cloning of the cDNA encoding a neuronal
A;Reference number: S21801; MUID:92235856
A;Accession: S21801
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A; Residues: 1914-1998, 'I' <SU2>
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N;Alternate names: myosin II
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A; Residues: 1-19
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Matches 62
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20.3%;
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5; Mismatches
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; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F. Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weldman, J.F.; McDonald, L. Nature 390, 364-370, 1997

A; Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S. Smith, H.O.; Woese, C.R.; Venter, J.C.
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaec A; Reference number: A69250; MUID:98049343

A; Accession: H69378
                                                                                                                  kinesin heavy chain - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision
C;Accession: I84737
                        R;Gudkov, A.V.; Kazarov, A.R.; Thimmapaya, R.; Axenovich, S.; Mazo, I.A.; Roninson, I.B. Proc. Natl. Acad. Sci. U.S.A. 91, 3744-3748, 1994
A;Title: Cloning mammalian genes by expression selection of genetic suppressor elements. A;Reference number: I49673; MUID:94224818
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Do.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
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C;Species: Archaeoglobus fulgidus
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 02-Feb-2001
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                                                                                                                                                                                                                                                                                                                          441 GRELDEEHRKN
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                                                                                                                                                                                                                                                                                                                                                                                                                                          CVSLKKEYENLKEARKATGELADRLKKDLVSSRSKLKTLNTELDQAKLELRSAQKDLQSA 205
                                                                                                                                                                                                                                                                                                                                                                    DOEITSLRKKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QAREEAHRLKCKMKTMEQIE------LLLQSQRSEVEEMIRDMGVGQSAVEQLAVY 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ERIED-LEKKAKEVKELKPKAERYSILEKLLSEINQALRDVEKREGDLTREAAGIQAQLK 325
                                                                                                                                                                                                                                                                                                                                                                                                               PDKVEKMYDLLSKAKEEEKEITEKLKK-LIAKKSSLKTRGAQLKKAVEELKSAERTCPVC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ESLREKLSEEVRNLESRLKELEEHKSRLESLRKQESSVLQEVRGLEEKLRELEKQLKEVV 266
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Pred. No. 0.11;
1; Mismatches
                                                                                                                                              02-Jul-1996 #text_change 13-Aug-1999
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irkness, E.F
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myosin heavy chain, nonmuscle (clone lambda-FMHC) - C;Species: Gallus gallus (chicken) C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #C;Accession: S06117
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S06117
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A; Residues: 1-881 <RES>
A; Cross-references: GB:L27153;
C; Genetics:
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A;Note: this translation is not annotated in GenBank entry GGMHCFC, C;Superfamily: myosin heavy chain; myosin motor domain homology F;1-303/Domain: myosin motor domain homology (fragment) <
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: not compared with conceptual translation A;Molecule type: mRNA A;Residues: 1-924 <KAT>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Reference number: A; Accession: S06117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Title:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Katsuragawa, Y.; Ya
Eur. J. Biochem. 184,
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mes 65; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Two distinct nonmuscle myosin-heavy-chain mRNAs
                                                                                                                                                                                                                DREKRDSQAIIDTLRDTLEERNATVESLQNALNKAEMLCSTLKK------QMKFL 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DASKEEVKEVLQA-----LEELAVNYDQKSQEVEDKTKEYELLSDELNQKSATLASIDA 535
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                                   DAQVQELTAKVTEGERLRVELAEKANKLQNELDNVSSLLEEAEKKGIKFAKDAASLESQL
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                                                                   -SEVEEMIRDMGVGQSAVEQLAVYCVSLKKEYEN----LKEARKA---
                                                                                                         RORHATALEELSEQLEQAKRFKANLEKNKOGLESDNKELACEVKVLOOVKAESEHKRKKL
                                                                                                                                             EQRQ----DETKQAREEAHRLK------CKMKTMEQIELLLQSQR---
                                                                                                                                                                               EKQKRDLSEELEALKTELEDTLDTTAAQQELRTKREQEVAELKKAIEEETKNHEAQIQEI
                                                                                                                                                                                                                                                  IEELKIQLAKKEEELQAALARGDEEAVQKNNALKVIRELQAQIAELQEDLESEKASRNKA 669
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ELQKLKEMTNHQKKRAAEMMASLLKDLAEIGIAVGNNDVKQPEGTGMIDEEFTVARLYIS 595
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57; Conser
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34, 611-616, 1989
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21.3%;
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                                                                                                                                                                                                                                                                                                                            58;
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                                                                                                                                                                                                                                                                                                                                           Score 157; DB Pred. No. 0.12;
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--TGELADRLKKDLVSSRSKLKTLNTE---LDQAKLELRSAQKDLQ---

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C; Species: Di
C; Date: 20-Se
C; Accession:
A; Molecule type: mRNA A; Residues: 1-2007 <TAK> A; Residues: 1-2007 <TAK> A; Cross-references: GB: M93676; NID: g212448; PIDN: AAA48988.1; A; Note: the sequence of residues 212-221 and 632-652 and the A; Accession: A43402
                                                                                                                                                                                                                                                    myosin heavy chain-B, neuronal - chicken
N;Contains: myosin ATPase (EC 3.6.1.32)
C;Species: Gallus gallus (chicken)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change
C;Accession: B43402; A43402
R;Takahashi, M.; Kawamoto, S.; Adelstein, R.S.
J. Biol. Chem. 267, 17864-17871, 1992
                                                                                                                                                                                                                                                                                                                                                                             RESULT
B43402
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A; Gene: abp
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A; Residues: 1-1738 <RIV>
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J. Cell Biol. 142, 735-750, 1998
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                                                                                                                                                                                                                                       for inserted sequences in
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F;88-82/Domain: myosin motor domain homology <a href="Months Fig. 178-185/Region: nucleotide-binding motif A (P-loop)">Months F:178-185/Region: nucleotide-binding motif A (P-loop)</a>
F:212-221/Region: alternatively spliced segment 1 #status experimental F;59-593/Region: actin binding #status predicted F:632-652/Region: actin binding #status predicted = #status experimental F:692-714/Region: actin binding #status predicted = #status experimental F:692-714/Region: actin binding #status predicted = #status experimental F:875-2007/Domain: coiled coil #status predicted = #status experimental F:875-1315/Region: 11ght meromyosin F:1316-2007/Region: 11ght meromyosin F:129/Modified site: N6, N6, N6 trimethyllysine (Lys) #status predicted F:184/Binding site: ATP (Lys) #status predicted F:194/Binding site: phosphate (Thr) (covalent) #status predicted F:1987/Binding site: phosphate (Ser) (covalent) #status predicted
C;Superfamily: myosin heavy chain; myosin motor domain c;Keywords: actin binding; ATP; coiled coil; hydrolase; F;92-775/Domain: myosin motor domain homology <MNOT> F:182-189/Region: nucleotide-binding motif A (P-loop) F;544-576/Region: actin binding #status predicted F;660-682/Region: actin binding #status predicted F;680-682/Region: actin binding #status predicted F;848-1227/Domain: coiled coil #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   myosin heavy chain II - Acanthamoeba castellanii
N;Contains: myosin ATPase (EC 3.6.1.32)
C;Species: Acanthamoeba castellanii
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 19-Jan-2001
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                                                                                                                                                                                                                                                                                                           A; Title: Complete nucleotide sequence and A; Reference number: A27224; MUID:87308395 A; Accession: A27224
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                                                                                                                                                                                                          C; Genetics:
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A; Residues: 1-1509 <HAM>
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Best Local Similarity
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Pred. No. 0.
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myosin heavy chain, smooth muscle, splice form 2 - rat (fragment)
C;Speciles: Rattus norvegicus (Norway rat)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 21-Jul-2000
C;Accession: S07537; S10449
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F:1248-1482/Domain: coiled coil #status predicted <CO2>
F:1248-1482/Domain: carboxyl-terminal <CBT>
F:133/Modified site: N6.N6.N6-trimethyllysine (Lys) #status
F:188/Binding site: ATP (Lys) #status predicted
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J. Mol. Biol. 210, 673-679, 1989
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A; Residues: 1-412 <BAB>
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                                                                                                         DLAQEEENVLDAEFLKNELDSVKAQLSQK-----DREKRDSQAIIDTLRDTLEE 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LNTELDQAKLELRSAQ------KDLQSADQEITSLRKKSDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VRANVDKQKKALEAKLTELEDQVTALDGQKNAAAAQAKTLKTQVDETKRRLEEAEASAAR 1196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DLAQEEENVLD---
              EQGNMEAMSDRVRKATLQAEQLSNELVTERSAAQKNESARQQLERQNKELRSKLQEVEGA
                                           RNATVESLQNALNKAEMLCSTLKKOMKFLEQRQDETKQAREEAHR--------
                                                                            ELMQLQEDLAAAERARKQADLEKEELAEELASSLSGRNTLQDEKRRLEARIAQLEEELEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LEGELERLEEELLTAQEARAAAEKNLDKANLELEELRQEADD 1298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LEKERKNALDEVAQLTADLDAERDSGAQQRRKLNTRISELQSELENAPKTGGASSEEVKR 1256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AR----RSEVEEMIRDMGVGQ-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EEKSGKEAASSKAKQLGQQLEDARSEVDSLKSKLSAAEKSLKTAKDQNRDLDEQLEDERT 1136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QKDREKRDSQAIIDTLRDTLEERNATVESLQNALNKAEMLCSTLKKQMKFLEQRQDETKQ 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DALADAENISETLRSKLKNTERGADDVRNELDDVTATKLQLEKTKKSLEEELAQTRAQLE 1076
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----SAVEQLAVYCVSLKKEYENLKEARKATGELADRLKKDLV-----SSRSKLKT 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity 20.159; Conservative
                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                 S10449
                                                                                                                                         Conservative
                                                                                                                                                        14.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14.6%;
                                                                                                                                                                                                                                                                                                                                                               Library,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          59;
                                                                                                                                         55;
                                                                                                                                                      Score 156; DB 2
Pred. No. 0.062;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 156.5; D
Pred. No. 0.22;
                                                                                                                                                                                                                                                                                                                                                             August 1989
                                                                                                                                         Mismatches
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                                                                                                                                                                      Length 412;
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                                                                                                                                       Gaps
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Yeast 12, 877-885, 1996
Yeast 12, 877-885, 1996
A; Title: Sequence and analysis of a 33 kb
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C;Date: 15-Feb-1996 #sequence_revision 01-Mar-1996
C;Accession: S60943; S67109; S71718
                                                                                                                                                                                                                                                                                                                                                               C;Function:
A;Description: suppressor of uso1-1 transport defect
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: EMBL:X92441; NID:g1050762; A;Note: the nucleotide sequence was submitted t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: EMBL:275124; NID:91420502; A;Experimental source: Strain S288C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-484 <BOY>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Reference number: S60938
A; Accession: S60943
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                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references:
A;Map position: 15R
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Accession: S71718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Reference number: S67104
A; Accession: S67109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             submitted to the Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: EMBL:X92441; NID:g1050762; PID:g1050768 R;Boyer, J.; Fairhead, C.; Gaillon, L.; Galisson, F.; Micha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Residues: 1-484 <GAL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Galisson, F.; Dujon, B. submitted to the EMBL Data Library,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RUD3 protein - yeast (Saccharomyces cerevisiae)
N;Alternate names: protein O5028; protein YOR21
                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Gene: SGD: RUD3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Residues: 1-484 <GAW>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: nucleic acid sequence not shown; translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Galisson,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
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                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                         Query Match
Best Local
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                                                                                                                                                                                                                               24 LKNELDSVKAQLSQKDREKRDSQAIIDTLRDTLEERN---ATVESLQNALNKAEMLCSTL
                                                                                                                                   KKQMKFLEQRQDETKQAREEAHRLKCKMKTMEQIELLLQSQRSEVEEMIRDMGVGQSAVE 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ITSLRKKSDDPP
                                                           QLAVYCVSLKKEYENLKEARKATGE-----
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DQAKLELRSAQKDLQSADQEITSLRKKSDD
                                                                                                               KEAQKQLEEVQEQLTE - - YESQNLKLKKK - - - - - -
                                                                                                                                                                                           LREEIERLKLELSHKKDQETPNEDFKNELANVIKERDEFKTQYDTLLSKISSMKSIFNKM
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                                                                                                                                                                                                                                                                       Similarity
51; Conser
                                     ---VTLNTELENLEKEQESTEEVFLEYESRIEALEDE-KHDIIEKHSKELNTYRKEK
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                                                                                                                                                                                                                                                                                         14.48;
                                                                                                                                                                                                                                                                       52;
                                                                                                                                                                                                                                                                   Score 155; DB 2
Pred. No. 0.083;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                            MIPS:YOR216c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein YOR216c;
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s of a 33 kb
218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      fragment
                                                                                                                                                                                                                                                                                                         DB 2;
                                                                       LADRLKKDLVSSRSK-LKTLNTEL
                                                                                                                 -LEATKTENSEL-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIDN:CAA63179.1; PID:g1050768 to the EMBL Data Library, October 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PID:e252397;
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                                                                                                                                                                                                                                                                       67;
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                                                                                                                                                                                                                                                                                                           Length 484;
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251

DQLNLQVQELMIILENNKQDISDLRTERDE

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microtubule binding protein D-CLIP-190 - f
C.Species: Drosophila melanogaster
C.Date: 13-Aug-1999 #sequence_revision 13-
C;Accession: T13030
R;Lantz, V.A.; Miller, K.G.
J. Cell Biol. 140, 897-910, 1998
A;Title: A class VI unconventional myosin
A;Reference number: 217588; MUID:98139549
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A; Residues: 1-1156 <AQF>
A; Cross-references: GB:AE000699; NID:g2983238; PIDN:AAC06839.1;
A; Experimental source: strain VF5
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 chromosome assembly protein homolog - Aquifex aeolicus (;Species: Aquifex aeolicus C;Species: Aquifex aeolicus C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 02-Jun-2000 C;Accession: B70356 R;Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Grand, B.;Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Grand, R;Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Grand, R;Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Grand, R;Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Grand, R;Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Grand, R;Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Grand, R;Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Grand, R;Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Grand, R;Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Grand, R;Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Grand, R;Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Grand, R;Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Grand, R;Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Grand, R;Deckert, G.; Warren, P.V.; Gaasterland, R;Deckert, G.; Warren, 
                                                                                                                                                                                                                                                                                                                                            A; Molecule type: mRNA
A; Residues: 1-1690 <LAN>
A; Cross-references: EMBL:AF041382; NID:g2773362; PID:g2773363; PIDN:AAB96783.1
A; Experimental source: strain Oregon R
C:Genetics:
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C; Superfamily:
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Matches 47
                                                                                                                                Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LKEEKEKLEKFKELQRIKRETEA-KILLKEKEKLLKERERILNELSSLRESLEDITFQIQ 265
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                                                       FDLAQEEENVLDAEFLKNELDSVKAQLSQKDREKRDSQAIIDTLRDTLEERNATVESLQN
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FQKKQSESEV---
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   ----HLQEIKAQNTQKDLELVESGESLKKLQQQLEEKTLGHEKLQA
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                                                                                                                             52;
                                                                                                                                                    Score 155;
Pred. No. 0.
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Pred. No. 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB
.2;
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.3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (Drosophila melanogaster)
                                                                                                                                                                                 Length 1690;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 1156;
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hypothetical protein B0432.6 - Caenorhabditis elegans C; Species: Caenorhabditis elegans C; Species: Caenorhabditis elegans C; Data: 15-Oct-1999 #sequence_revision 15-Oct-1999 #tc; Accession: T25454 R; Henkhaus, J.; Wohldmann, P. submitted to the EMBL Data Library, December 1996 submitted to the EMBL Data Library, December 1996 A; Description: The sequence of C. elegans cosmid B043;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Qy
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A;Gene: CESP:B0432.6
A;Map position: 2
A;Introns: 104/3; 190/3;
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A; Experimental source:
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A; Residues: 1-380 <HEN>
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  333 LSDRERDLNAKNLEIDRLKLDLDAARRNLQKLEQ
                                    175 VSSRSK-LKTLNTELDQAKLELRSAQKDLQSADQ
                                                                                288 DLELKNKQSDMERALLQI----SAAEQKAA----KKELE-LIEAEKHL----
                                                                                                                       115 ELLLQSQRSEVEEMIRDMGVGQSAVEQLAVYCVSLKKEYENLKEARKATGELADRLKKDL 174
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                                                                                                                                                                                                        59
                                                                                                                                                                                                                                                                       2 TIINKLFFDLAQEEENVLDAE--FLKN-ELDSVKAQLSQKDREKRDSQAIIDTLRDTLEE 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QITKLKSEVEETQAALSSYHTDVESKTKQLEAANAALEKVNKEYAESRAEASD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ---RLKKDLVSSRSKLKTLNTELDQAKLELRSAQKDLQSADQEITSLRKKSDD
                                                                                                                                                               RN--VHTAQNEISKLNTELAQSVTRIELFLAENR--ELKQEFEE-KVVECEVLKEHIRQI
                                                                                                                                                                                                        RNATVESLQNALNK--AEMLCSTLKKQMKFLEQRQDETKQAREEAHRLKCKM--KTMEQI 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EGSKTVAKLHDETSQLKSQAEETQSELKSTESNLEAKSKQLEAANGSLEEEAKKSGQLQE
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                                                                                                                                                                                                                                                                                                                                                    Similarity
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                                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                 211/1; 283/3; 304/3; 325/3
                                                                                                                                                                                                                                                                                                                                                  14.4%;
31.3%;
                                                                                                                                                                                                                                                                                                                             47; Mismatches
                                                                                                                                                                                                                                                                                                                                                  Score 154.5; DB Pred. No. 0.069;
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366
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                                                                                -KLYESR 332
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hypothetical protein F59A2.6 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 29-Oct-1999
C;Accession: T22976; T23157
R;Lightning, J.
R;Lightning, J.
Submitted to the EMBL Data Library, June 1994
A;Reference number: Z19645
A;Accession: T22976
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1133 <WIL>
A;Residues: 1-1133 <WIL>
A;Coss-references: EMBL:Z34801; PIDN:CAA84332.1; GSPDB:GN00021; CESP:F59A2
A;Experimental source: clone F59A2
R;Burton, J.
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myosin heavy chain 3, muscle - fruit fly (Drosophila melanogaster) (fragment) (;Species: Drosophila melanogaster C;Date: 28-Mar-1991 #sequence_revision 28-Mar-1991 #text_change 20-Jun-2000 C;Accession: C35815 R;Collier, V.L.; Kronert, W.A.; O'Donnell, P.T.; Edwards, K.A.; Bernstein, S.; Genes Dev. 4, 885-995, 1990 A;Title: Alternative myosin hinge regions are utilized in a tissue-specific fa A;Reference number: A35815; MUID:90346288
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                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-1175 <COL>
A; Cross-references: EMBL:X53155; NID:g8219; PIDN:CAA37308.1; PID:g2546936
A; Note: the authors translated the codon TGC for residue 649 as Lys, and C; Genetics:
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C:Superfamily: myosin heavy chain; myosin motor domain
C:Keywords: ATP
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A; Introns: 13/2; 43/3; 107/3; 413/3; 492/3; 567/3;
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Best Local
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                                     124
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                                                                                                                                                                 10 DLAQEEENVLD--AEFLKNELDSVKAQLSQKDREKRDSQAIIDTLRDTLEERNATVESLQ
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                                                                                                                                                                                                                                         Local
                                                                                                      NALNKAEMLCSTLKKOMKFL----EQRODETKQAREEAHRLKCKMKTMEQIELLLQSQRS
                                                                                                                                            DDAREQLGISERRANALQNELEESRTLLEQADRGRRQAEQELADAHEQLNEVSAQNASIS
ALEQQIKELQVRLDEAEANALKGGKKAIQKLEQRVRELENELDGEQRRHADAQKNLRKSE 1082
                                   EVEEMIRDMGV--
                                                                    AAKRKLESELQTLHSDLDELLNEAKNSEEKAKKAMVDAARLADELRAEQDHAQTQEKLRK 1022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    - IENLKKDAENERN-LKTALESDESSAISEITKQMEAAKKELEASEKEKSELREQMD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LADRLKKDLVSSRSKLKTL----NTELDQAKLELRSAQKDLQSADQEITSLRKKSD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IQELTEKLEESEKETSTAKTELEAVSKKLDSSETSLKEFSDMIEAMKIQLINCEKQKDEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VESLQNALNKAEMLCSTLKKQMKFLEQRQDETKQAREE-----AHRLKCKMKTMEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EESKKVLESEKQAFENEKEQEREEQLAKAMEKLNSEQNILDEVTKKLEQSEEEVLAARGA 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IELLLQSQRSEVEEMIRDMGVGQ------SAVEQLAVYCVSLKKEYENLKEARKATGE 165
                                                                                                                                                                                                                       59;
                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                       14.4%; 22.8%;
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24.18;
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                                                                                                                                                                                                                      56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62;
                                  GQSAVEQLAVYCVSLKKEYE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIDN:CAA91344.1;
                                                                                                                                                                                                                    Score 154.5; D
Pred. No. 0.22;
6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 154.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               No. 0.21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               utilized in a tissue-specific fashion
                                                                                                                                                                                                                                                          DΒ
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                                                                                                                                                                                                                      91;
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                                                                                                                                                                                                                                                                                                                              homology
                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                      Length 1175;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      710/3;
                                                                                                                                                                                                                      53;
                                  -NLKEAR 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      738/3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    217
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                                                                                                                                                                                                                                                                                                                                                                                                        AAG
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Genes Dev. 4, 885-895, 1990
A:Title: Alternative myosin hinge regions A;Reference number: A35815; MUID:90346288
A;Accession: D35815
A:Accession: D35815
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C; Keywords:
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A; Residues: 1-1175 <COL>
A; Cross-references: EMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           myosin heavy chain 4, muscle - fruit fly (Drosophila melanogaster) (fragment) C;Species: Drosophila melanogaster C;Date: 28-Mar-1991 #sequence_revision 28-Mar-1991 #text_change 13-Feb-1998 C;Accession: D35815
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                                                                                                                                                                                                                                                                                                                                                                                                         A; Status: preliminary
                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                    Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                    Genetics:
                               1023 ALEQQIKELQVRLDEAEANALKGGKKAIQKLEQRVRELENELDGEQRRHADAQKNLRKSE 1082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1143 EAEERADLAEQAISKFRAK
    161
                                                           124
                                                                                                                                              903
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                                                                                                                   89
                                                                                                                                                                          10 DLAQEEENVLD--AEFLKNELDSVKAQLSQKDREKRDSQAIIDTLRDTLEERNATVESLQ 67
  KATGELA-----DRLK-----KDLVSS-RSKLKTLNTELDQAK------LELRSAQKDLQ
                                                                                                                NALNKAEMLCSTLKKQMKFL----EQRQDETKQAREEAHRLKCKMKTMEQIELLLQSQRS
                                                                                                                                            DDAREQLGISERRANALQNELEESRTLLEQADRGRRQAEQELADAHEQLNEVSAQNASIS 962
                                                           EVEEMIRDMGV----
                                                                                      AAKRKLESELQTLHSDLDELLNEAKNSEEKAKKAMVDAARLADELRAEQDHAQTQEKLRK 1022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          S-----ADQEITSLRKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RRVKELSFQSEEDRKNHERMQDLVDKLQQKIKTYKRQIEEAEEIAALNLAKFRKAQQELE 1142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     l Similarity
59; Conserv
                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                 EMBL: X53155
                                                                                                                                                                                                                    14.48; 22.88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              W.A.; O'Donnell,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1161
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                                                                                                                                                                                                                                                                                                                                                  the codon
                                                                                                                                                                                                       56;
                                                          -GQSAVEQLAVYCVSLKKEYE---
                                                                                                                                                                                                    Score 154.5; 1
Pred. No. 0.22
66; Mismatches
                                                                                                                                                                                                                                                                                         myosin
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                                                        NLKEAR 160
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    203
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RESULT 39
A35815
A35816
C;Species: Drosophila melanogaster
C;Species: Drosophila melanogaster
C;Date: 12-Oct-1990 #sequence_revision 28-Mar-1991 #text_change 20-Jun-2000
C;Accession: A35815
R;Collier, V.L.; Kronert, W.A.; O'Donnell, P.T.; Edwards, K.A.; Bernstein, S.I.
Genes Dev. 4, 885-895, 1990
A;Title: Alternative myosin hinge regions are utilized in a tissue-specific fashion A;Reference number: A35815
A;Accession: A35815
A;Accession: A35815
A;Accession: A35815
A;Residues: 1-1201 <COL>
A;Cross-references: EMBL:X53155; NID:g8219; PIDN:CAA37310.1; PID:g2546938

8 80 80

1143

EAEERADLAEQAISKFRAK

204

s-

----ADQEITSLRKK

1083

RRVKELSFQSEEDRKNHERMQDLVDKLQQKIKTYKRQIEEAEEIAALNLAKFRKAQQELE

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A;Note: the authors translated the codon TGC for residue 649 as Lys, and AAG for residue C;Genetics:
A;Gene: FlyBase:Mhc
A;Cross-references: FlyBase:FBgn0002741
C;Superfamily: myosin heavy chain; myosin motor domain homology
C;Keywords: ATP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               myosin heavy chain 2, muscle - fruit fly (Drosophila melanogaster) (fragment) C;Species: Drosophila melanogaster
C;Species: Drosophila melanogaster
C;Date: 28-Mar-1991 #sequence_revision 28-Mar-1991 #text_change 20-Jun-2000
C;Accession: B35815
R;Collier, V.L.; Kronert, W.A.; O'Donnell, P.T.; Edwards, K.A.; Bernstein, S.I.
Genes Dev. 4, 885-895, 1990
A;Title: Alternative myosin hinge regions are utilized in a tissue-specific fashion that A;Accession: B35815; MUID:90346288
A;Accession: B35815
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A; Molecule type: DNA
A; Residues: 1-1201 <COL>
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C;Superfamily: myosin heavy chain; myosin motor domain homology
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Best Local S
Matches 59
                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 22.8
Conservative
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                                                1023 ALEQQIKELQVRLDEAEANALKGGKKAIQKLEQRVRELENELDGEQRRHADAQKNLRKSE 1082
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                                                                                                124 EVEEMIRDMGV--
161 KATGELA-----DRLK----KDLVSS-RSKLKTLNTELDQAK-----LELRSAQKDLQ 203
                                                                                                                                                                                                                                            903 DDAREQLGISERRANALQNELEESRTLLEQADRGRRQAEQELADAHEQLNEVSAQNASIS 962
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    68 NALNKAEMLCSTLKKOMKFL----EQRODETKOAREEAHRLKCKMKTMEQIELLLOSORS 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
nes 59; Conserv
                                                                                                                                                                                                                                                                                        10 DLAQEEENVLD--AEFLKNELDSVKAQLSQKDREKRDSQAIIDTLRDTLEERNATVESLQ 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10 DLAQEEENVLD--AEFLKNELDSVKAQLSQKDREKRDSQAIIDTLRDTLEERNATVESLQ 67
                                                                                                                                                                                            68 NALNKAEMLCSTLKKOMKFL----EQRODETKOAREEAHRLKCKMKTMEQIELLLQSQRS 123
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                                                                                                                                              AAKRKLESELQTLHSDLDELLNEAKNSEEKAKKAMVDAARLADELRAEQDHAQTQEKLRK 1022
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                                                                                                                                                                                                                                                                                                                                                                  14.4%; Score 154.5; D
22.8%; Pred. No. 0.22;
                                                                                                                                                                                                                                                                                                                                             56;
                                                                                              -GQSAVEQLAVYCVSLKKEYE--
                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                         DB 2;
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                                                                                              -NLKEAR 160
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Db 1083 RRVKELSFQSBEDRKNHERMODLVDKLQQKIKTYKRQIEEAEBIAALNLAKFRKAQQELE 1142

Qy 204 S-----ADQEITSLRKK 215
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Db 1143 EAEERADLAEQAISKFRAK 1161

Search completed: September 4, 2002, 16:13:04 Job time: 3248 sec